

SEQUENCE SEARCH SUMMARY

10/733, 776

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 22, 2005, 21:08:08 ; Search time 10887 Seconds
(without alignments)
6889.747 Million cell updates/sec

Title: US-10-733-776-1
Perfect score: 1548
Sequence: 1 tcgcgatctggtactgtaag.....tgatcgggtccgaagaagatc 1548

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result | No. | Score | Match | Length | DB | ID | Description |
|--------|-----|-------|-------|--------|----|-----------|--------------------|
| | 1 | 1548 | 100.0 | 1548 | 6 | CQ849491 | CQ849491 Sequence |
| c | 2 | 1548 | 100.0 | 110000 | 1 | U00096_44 | Continuation (45 o |

| | | | | | | | | | |
|---|----|--------|-------|--------|---|-------------|---------------|--------------------|----------|
| c | 3 | 1548 | 100.0 | 338534 | 1 | ECOUW93 | 1995 Blattner | U14003 Escherichia | seq only |
| c | 4 | 1532 | 99.0 | 243184 | 1 | AP002568 | 2000 Genome | AP002568 Escherich | |
| | 5 | 1477.6 | 95.5 | 12561 | 1 | AE015432 | Genome 2002 | AE015432 Shigella | |
| | 6 | 1477.6 | 95.5 | 225944 | 1 | AE016993 | " | AE016993 Shigella | |
| c | 7 | 1458.4 | 94.2 | 306118 | 1 | AE016771 | " | AE016771 Escherich | |
| c | 8 | 1075 | 69.4 | 13970 | 1 | AE005657 | 11 2001 | AE005657 Escherich | |
| c | 9 | 975.6 | 63.0 | 1411 | 6 | CQ849499 | Appl 2004 | CQ849499 Sequence | |
| | 10 | 962.2 | 62.2 | 221961 | 2 | AC147436 | seq only | AC147436 Gallus ga | |
| | 11 | 731 | 47.2 | 151040 | 2 | AC020827 | 2000 model | AC020827 Mus muscu | |
| c | 12 | 706.4 | 45.6 | 249050 | 1 | AL627283 | genome 2003 | AL627283 Salmonell | |
| c | 13 | 706.4 | 45.6 | 284233 | 1 | AE016849 | " | AE016849 Salmonell | |
| c | 14 | 704.8 | 45.5 | 20095 | 1 | AE008909 | " | AE008909 Salmonell | |
| | 15 | 622 | 40.2 | 622 | 6 | CQ849497 | Appl | CQ849497 Sequence | |
| | 16 | 612 | 39.5 | 612 | 6 | CQ849498 | | CQ849498 Sequence | |
| c | 17 | 601 | 38.8 | 219912 | 2 | AC020855 | | AC020855 Mus muscu | |
| c | 18 | 516.6 | 33.4 | 11096 | 1 | AE005656 | | AE005656 Escherich | |
| | 19 | 489.8 | 31.6 | 1410 | 1 | ECOPYRBIA | | K01472 E.coli pyrB | |
| c | 20 | 463.4 | 29.9 | 110000 | 1 | BX950851_04 | | Continuation (5 of | |
| c | 21 | 449.8 | 29.1 | 51626 | 2 | AC009151 | | AC009151 Homo sapi | |
| c | 22 | 413.8 | 26.7 | 110000 | 2 | AC073744_1 | | Continuation (2 of | |
| | 23 | 405.6 | 26.2 | 110000 | 1 | BX936398_41 | | Continuation (42 o | |
| | 24 | 402 | 26.0 | 10029 | 1 | AE013616 | | AE013616 Yersinia | |
| | 25 | 402 | 26.0 | 216050 | 1 | AJ414157 | | AJ414157 Yersinia | |
| | 26 | 402 | 26.0 | 229338 | 1 | AE017142 | | AE017142 Yersinia | |
| | 27 | 367.2 | 23.7 | 1812 | 1 | STPYRBIG | | X05641 S.typhimuri | |
| | 28 | 367 | 23.7 | 1333 | 1 | AF095578 | | AF095578 Salmonell | |
| | 29 | 353 | 22.8 | 10465 | 1 | AE004321 | | AE004321 Vibrio ch | |
| | 30 | 345 | 22.3 | 465 | 6 | AR384860 | | AR384860 Sequence | |
| c | 31 | 337 | 21.8 | 300169 | 1 | AE016801 | | AE016801 Vibrio vu | |
| | 32 | 333.8 | 21.6 | 248650 | 1 | AP005341 | | AP005341 Vibrio vu | |
| | 33 | 317.8 | 20.5 | 89934 | 2 | AC008867 | | AC008867 Homo sapi | |
| | 34 | 313.4 | 20.2 | 387 | 6 | CQ849501 | | CQ849501 Sequence | |
| | 35 | 307.4 | 19.9 | 349907 | 1 | BX571874 | | BX571874 Photorhab | |
| | 36 | 302.2 | 19.5 | 1760 | 1 | AF190426 | | AF190426 Erwinia h | |
| | 37 | 298.6 | 19.3 | 1945 | 1 | SMAPYRBI | | J05033 Serratia ma | |
| c | 38 | 296.8 | 19.2 | 4989 | 1 | STU07843 | | U07843 Salmonella | |
| | 39 | 292 | 18.9 | 423 | 6 | AR384790 | | AR384790 Sequence | |
| | 40 | 280.6 | 18.1 | 296650 | 1 | AP005082 | | AP005082 Vibrio pa | |
| | 41 | 252.6 | 16.3 | 1224 | 6 | AR384827 | | AR384827 Sequence | |
| c | 42 | 251.8 | 16.3 | 2775 | 6 | AR384942 | | AR384942 Sequence | |
| | 43 | 219.2 | 14.2 | 110000 | 6 | AR409405_3 | | Continuation (4 of | |
| | 44 | 219.2 | 14.2 | 110000 | 6 | AR409405_4 | | Continuation (5 of | |
| | 45 | 219.2 | 14.2 | 110000 | 6 | BD061520_3 | | Continuation (4 of | |

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OM nucleic - nucleic search, using sw model

Run on: May 22, 2005, 12:14:12 ; Search time 1262 Seconds
(without alignments)
7261.299 Million cell updates/sec

Title: US-10-733-776-1
Perfect score: 1548
Sequence: 1 tcgcgatctggtactgtaag.....tgatcgggtccgaagaagatc 1548

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Match | Query Length | DB ID | Description |
|------------|-------|---------|--------------|-------------|------------------------------------|
| 1 | 561.2 | 36.3 | 1436 | 5 AAS93208 | 2002 Aas93208 DNA encod human |
| 2 | 462 | 29.8 | 462 | 13 ADT48924 | 2002 X Adt48924 Bacterial in plant |
| 3 | 414 | 26.7 | 2913 | 5 AAS89034 | 2001 Aas89034 DNA encod human |

| | | | | | | | | | |
|---|----|-------|------|--------|----|----------|------|--------------------|-------|
| c | 4 | 414 | 26.7 | 2913 | 5 | AAS73466 | 2002 | Aas73466 DNA encod | human |
| c | 5 | 391 | 25.3 | 2697 | 8 | ACA18785 | 2002 | Aca18785 Prokaryot | |
| c | 6 | 391 | 25.3 | 2697 | 13 | ADT48923 | | Adt48923 Bacterial | |
| c | 7 | 365 | 23.6 | 1267 | 5 | AAS89802 | | Aas89802 DNA encod | |
| c | 8 | 365 | 23.6 | 1267 | 5 | AAS90167 | | Aas90167 DNA encod | |
| c | 9 | 365 | 23.6 | 1267 | 5 | AAS89259 | | Aas89259 DNA encod | |
| c | 10 | 365 | 23.6 | 3678 | 5 | AAS91989 | | Aas91989 DNA encod | |
| | 11 | 345 | 22.3 | 465 | 11 | ACH95794 | | Ach95794 Klebsiell | |
| c | 12 | 330 | 21.3 | 3117 | 5 | AAS69095 | | Aas69095 DNA encod | |
| c | 13 | 330 | 21.3 | 3117 | 5 | AAS89240 | | Aas89240 DNA encod | |
| c | 14 | 330 | 21.3 | 4942 | 5 | AAS89816 | | Aas89816 DNA encod | |
| c | 15 | 330 | 21.3 | 4944 | 5 | AAS89273 | | Aas89273 DNA encod | |
| c | 16 | 330 | 21.3 | 4944 | 5 | AAS90181 | | Aas90181 DNA encod | |
| | 17 | 322.4 | 20.8 | 2481 | 5 | AAS90282 | | Aas90282 DNA encod | |
| c | 18 | 307.4 | 19.9 | 110000 | 10 | ACF67367 | 39 | Continuation (40 o | |
| | 19 | 307.4 | 19.9 | 110000 | 10 | ACF65388 | 08 | Continuation (9 of | |
| c | 20 | 295 | 19.1 | 2709 | 8 | ACA51279 | | Aca51279 Prokaryot | |
| | 21 | 292 | 18.9 | 423 | 11 | ACH95724 | | Ach95724 Klebsiell | |
| c | 22 | 291.8 | 18.9 | 2709 | 8 | ACA52121 | | Aca52121 Prokaryot | |
| c | 23 | 284.8 | 18.4 | 1541 | 8 | ACA49041 | | Aca49041 Prokaryot | |
| c | 24 | 258.6 | 16.7 | 4752 | 5 | AAS89807 | | Aas89807 DNA encod | |
| c | 25 | 258.6 | 16.7 | 4752 | 5 | AAS89264 | | Aas89264 DNA encod | |
| c | 26 | 258.6 | 16.7 | 4752 | 5 | AAS73420 | | Aas73420 DNA encod | |
| c | 27 | 258.6 | 16.7 | 4752 | 5 | AAS94398 | | Aas94398 DNA encod | |
| c | 28 | 258.6 | 16.7 | 4752 | 5 | AAS90172 | | Aas90172 DNA encod | |
| | 29 | 258.6 | 16.7 | 4752 | 5 | AAS93795 | | Aas93795 DNA encod | |
| c | 30 | 255.8 | 16.5 | 2706 | 8 | ACA31992 | | Aca31992 Prokaryot | |
| | 31 | 252.6 | 16.3 | 1224 | 11 | ACH95761 | | Ach95761 Klebsiell | |
| c | 32 | 251.8 | 16.3 | 2775 | 11 | ACH95876 | | Ach95876 Klebsiell | |
| c | 33 | 251 | 16.2 | 2706 | 8 | ACA35909 | | Aca35909 Prokaryot | |
| | 34 | 235.8 | 15.2 | 465 | 10 | ACF70839 | | Acf70839 Photorhab | |
| | 35 | 231.4 | 14.9 | 387 | 10 | ACF70838 | | Acf70838 Photorhab | |
| | 36 | 225 | 14.5 | 1764 | 5 | AAS90169 | | Aas90169 DNA encod | |
| | 37 | 225 | 14.5 | 1764 | 5 | AAS89261 | | Aas89261 DNA encod | |
| | 38 | 225 | 14.5 | 1764 | 5 | AAS89804 | | Aas89804 DNA encod | |
| | 39 | 224.4 | 14.5 | 462 | 13 | ADS45443 | | Ads45443 Bacterial | |
| | 40 | 219.2 | 14.2 | 110000 | 6 | ABA92787 | 3 | Continuation (4 of | |
| | 41 | 219.2 | 14.2 | 110000 | 6 | ABA92787 | 4 | Continuation (5 of | |
| | 42 | 207.2 | 13.4 | 456 | 13 | ADS45703 | | Ads45703 Bacterial | |
| | 43 | 204.4 | 13.2 | 393 | 11 | ACH95569 | | Ach95569 Klebsiell | |
| | 44 | 204.2 | 13.2 | 480 | 10 | ADF01255 | | Adf01255 Bacterial | |
| | 45 | 197 | 12.7 | 2590 | 3 | AAC79620 | | Aac79620 Virulence | |

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OM nucleic - nucleic search, using sw model

Run on: May 22, 2005, 23:18:27 ; Search time 409 Seconds
(without alignments)
6193.047 Million cell updates/sec

Title: US-10-733-776-1
Perfect score: 1548
Sequence: 1 tcgcatctggtactgtaag.....tgatcgggtccgaagaagatc 1548

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Match | Query Length | DB | ID | Description |
|------------|-------|---------|--------------|----|---------------------|--------------------|
| 1 | 345 | 22.3 | 465 | 4 | US-09-489-039A-1589 | Sequence 1589, Ap |
| 2 | 292 | 18.9 | 423 | 4 | US-09-489-039A-1519 | Sequence 1519, Ap |
| 3 | 252.6 | 16.3 | 1224 | 4 | US-09-489-039A-1556 | Sequence 1556, Ap |
| c 4 | 251.8 | 16.3 | 2775 | 4 | US-09-489-039A-1671 | Sequence 1671, Ap |
| 5 | 219.2 | 14.2 | 640681 | 4 | US-09-790-988-1 | Sequence 1, Appli |
| 6 | 204.4 | 13.2 | 393 | 4 | US-09-489-039A-1364 | Sequence 1364, Ap |
| 7 | 204.2 | 13.2 | 480 | 4 | US-09-543-681A-1540 | Sequence 1540, Ap |
| 8 | 197 | 12.7 | 2590 | 4 | US-09-809-665A-78 | Sequence 78, Appli |
| 9 | 194.2 | 12.5 | 386 | 4 | US-09-809-665A-174 | Sequence 174, App |
| 10 | 188.2 | 12.2 | 1830121 | 4 | US-09-557-884-1 | Sequence 1, Appli |
| 11 | 188.2 | 12.2 | 1830121 | 4 | US-09-643-990A-1 | Sequence 1, Appli |

K pneumoniae

Handwritten arrow pointing from 'Seulaw' to the bottom of the table.

| | | | | | | | |
|---|----|-------|------|--------|---|----------------------|-------------------|
| c | 12 | 173.4 | 11.2 | 2442 | 4 | US-09-328-352-3295 | Sequence 3295, Ap |
| | 13 | 171.4 | 11.1 | 402 | 4 | US-09-543-681A-1492 | Sequence 1492, Ap |
| c | 14 | 153.2 | 9.9 | 2493 | 4 | US-09-252-991A-10571 | Sequence 10571, A |
| c | 15 | 153.2 | 9.9 | 2967 | 4 | US-09-252-991A-10675 | Sequence 10675, A |
| | 16 | 153.2 | 9.9 | 3027 | 4 | US-09-252-991A-10492 | Sequence 10492, A |
| c | 17 | 107.8 | 7.0 | 1218 | 4 | US-09-252-991A-7267 | Sequence 7267, Ap |
| | 18 | 104.6 | 6.8 | 468 | 4 | US-09-252-991A-7435 | Sequence 7435, Ap |
| c | 19 | 98.8 | 6.4 | 536165 | 4 | US-09-214-808-1 | Sequence 1, Appli |
| | 20 | 91 | 5.9 | 786 | 4 | US-09-489-039A-1447 | Sequence 1447, Ap |
| | 21 | 88.6 | 5.7 | 414 | 4 | US-09-543-681A-1634 | Sequence 1634, Ap |
| | 22 | 88.4 | 5.7 | 405 | 4 | US-09-134-000C-3050 | Sequence 3050, Ap |
| c | 23 | 85.4 | 5.5 | 2858 | 3 | US-09-221-017B-1013 | Sequence 1013, Ap |
| c | 24 | 85.4 | 5.5 | 21040 | 3 | US-08-961-527-55 | Sequence 55, Appl |
| | 25 | 83 | 5.4 | 456 | 4 | US-09-540-236-881 | Sequence 881, App |
| c | 26 | 81.6 | 5.3 | 94750 | 4 | US-09-596-002-38 | Sequence 38, Appl |
| | 27 | 80.6 | 5.2 | 402 | 4 | US-09-107-433-1225 | Sequence 1225, Ap |
| c | 28 | 80 | 5.2 | 1270 | 1 | US-08-915-003-8 | Sequence 8, Appli |
| c | 29 | 80 | 5.2 | 1270 | 2 | US-08-642-247-8 | Sequence 8, Appli |
| | 30 | 78.8 | 5.1 | 381 | 4 | US-09-583-110-650 | Sequence 650, App |
| | 31 | 78.8 | 5.1 | 4718 | 4 | US-08-956-171E-299 | Sequence 299, App |
| | 32 | 78.8 | 5.1 | 4718 | 4 | US-08-781-986A-299 | Sequence 299, App |
| c | 33 | 72.8 | 4.7 | 400 | 3 | US-08-976-259-134 | Sequence 134, App |
| c | 34 | 72.8 | 4.7 | 400 | 4 | US-09-956-004-134 | Sequence 134, App |
| c | 35 | 72.6 | 4.7 | 3466 | 3 | US-09-027-166-10 | Sequence 10, Appl |
| | 36 | 72 | 4.7 | 402 | 3 | US-09-134-001C-512 | Sequence 512, App |
| | 37 | 72 | 4.7 | 6318 | 3 | US-09-453-702B-230 | Sequence 230, App |
| | 38 | 68.4 | 4.4 | 14077 | 4 | US-09-902-540-1109 | Sequence 1109, Ap |
| | 39 | 68 | 4.4 | 396 | 4 | US-09-902-540-2456 | Sequence 2456, Ap |
| c | 40 | 66.8 | 4.3 | 2667 | 4 | US-09-134-000C-2481 | Sequence 2481, Ap |
| | 41 | 63.4 | 4.1 | 2605 | 3 | US-09-651-656-104 | Sequence 104, App |
| | 42 | 63.4 | 4.1 | 2605 | 3 | US-09-650-855-104 | Sequence 104, App |
| | 43 | 62.6 | 4.0 | 444 | 4 | US-09-328-352-1962 | Sequence 1962, Ap |
| | 44 | 60.2 | 3.9 | 1017 | 3 | US-09-125-265-1 | Sequence 1, Appli |
| c | 45 | 58.4 | 3.8 | 5629 | 3 | US-09-453-702B-243 | Sequence 243, App |

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OM nucleic - nucleic search, using sw model

Run on: May 23, 2005, 03:05:23 ; Search time 6575 Seconds
(without alignments)
1443.777 Million cell updates/sec

Title: US-10-733-776-1
Perfect score: 1548
Sequence: 1 tcgcgatctggtactgtaag.....tgatcgggtccgaagaagatc 1548

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5695437 seqs, 3066160638 residues

Total number of hits satisfying chosen parameters: 11390874

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result | | % | Query | | | | | |
|--------|-------|-------|--------|---------|----|----------------------|-------------|-------------------|
| No. | Score | Match | Length | DB | ID | | Description | |
| | 1 | 1548 | 100.0 | 1548 | 18 | US-10-733-776-1 | App1 | Sequence 1, Appli |
| c | 2 | 975.6 | 63.0 | 1411 | 18 | US-10-733-776-9 | " | Sequence 9, Appli |
| | 3 | 622 | 40.2 | 622 | 18 | US-10-733-776-7 | " | Sequence 7, Appli |
| | 4 | 612 | 39.5 | 612 | 18 | US-10-733-776-8 | " | Sequence 8, Appli |
| | 5 | 462 | 29.8 | 462 | 17 | US-10-369-493-47362 | 2003 x | Sequence 47362, A |
| c | 6 | 391 | 25.3 | 2697 | 17 | US-10-369-493-47361 | " | Sequence 47361, A |
| c | 7 | 391 | 25.3 | 2697 | 17 | US-10-282-122A-6655 | 2004 | Sequence 6655, Ap |
| | 8 | 313.4 | 20.2 | 387 | 18 | US-10-733-776-11 | " | Sequence 11, Appl |
| c | 9 | 295 | 19.1 | 2709 | 17 | US-10-282-122A-39149 | | Sequence 39149, A |
| c | 10 | 291.8 | 18.9 | 2709 | 17 | US-10-282-122A-39991 | | Sequence 39991, A |
| c | 11 | 284.8 | 18.4 | 1541 | 17 | US-10-282-122A-36911 | | Sequence 36911, A |
| c | 12 | 255.8 | 16.5 | 2706 | 17 | US-10-282-122A-19862 | | Sequence 19862, A |
| c | 13 | 251 | 16.2 | 2706 | 17 | US-10-282-122A-23779 | | Sequence 23779, A |
| | 14 | 224.4 | 14.5 | 462 | 17 | US-10-369-493-23873 | | Sequence 23873, A |
| | 15 | 219.2 | 14.2 | 640681 | 9 | US-09-790-988-1 | | Sequence 1, Appli |
| | 16 | 207.2 | 13.4 | 456 | 17 | US-10-369-493-24133 | | Sequence 24133, A |
| | 17 | 197 | 12.7 | 2590 | 11 | US-09-809-665A-78 | | Sequence 78, Appl |
| | 18 | 197 | 12.7 | 2590 | 18 | US-10-854-299-78 | | Sequence 78, Appl |
| | 19 | 194.2 | 12.5 | 386 | 11 | US-09-809-665A-174 | | Sequence 174, App |
| | 20 | 194.2 | 12.5 | 386 | 18 | US-10-854-299-174 | | Sequence 174, App |
| c | 21 | 188.4 | 12.2 | 2514 | 17 | US-10-369-493-37708 | | Sequence 37708, A |
| | 22 | 188.2 | 12.2 | 1830121 | 17 | US-10-329-670-1 | | Sequence 1, Appli |
| | 23 | 188.2 | 12.2 | 1830121 | 18 | US-10-158-865-1 | | Sequence 1, Appli |
| c | 24 | 170.4 | 11.0 | 2754 | 17 | US-10-282-122A-8510 | | Sequence 8510, Ap |
| | 25 | 163.8 | 10.6 | 597 | 18 | US-10-363-345A-10927 | | Sequence 10927, A |
| c | 26 | 163.8 | 10.6 | 597 | 18 | US-10-363-345A-10928 | | Sequence 10928, A |
| | 27 | 163.8 | 10.6 | 597 | 19 | US-10-363-483A-10927 | | Sequence 10927, A |
| c | 28 | 163.8 | 10.6 | 597 | 19 | US-10-363-483A-10928 | | Sequence 10928, A |
| c | 29 | 162.6 | 10.5 | 597 | 18 | US-10-363-345A-10925 | | Sequence 10925, A |
| | 30 | 162.6 | 10.5 | 597 | 18 | US-10-363-345A-10926 | | Sequence 10926, A |
| c | 31 | 162.6 | 10.5 | 597 | 19 | US-10-363-483A-10925 | | Sequence 10925, A |
| | 32 | 162.6 | 10.5 | 597 | 19 | US-10-363-483A-10926 | | Sequence 10926, A |
| c | 33 | 153.2 | 9.9 | 2712 | 17 | US-10-282-122A-30551 | | Sequence 30551, A |
| c | 34 | 146.8 | 9.5 | 2760 | 17 | US-10-282-122A-32143 | | Sequence 32143, A |
| c | 35 | 138.6 | 9.0 | 2649 | 17 | US-10-282-122A-12198 | | Sequence 12198, A |
| c | 36 | 134 | 8.7 | 2700 | 17 | US-10-282-122A-41612 | | Sequence 41612, A |
| c | 37 | 128.8 | 8.3 | 684707 | 17 | US-10-398-221-9 | | Sequence 9, Appli |
| | 38 | 128.8 | 8.3 | 3011208 | 17 | US-10-398-221-2058 | | Sequence 2058, Ap |
| c | 39 | 126.8 | 8.2 | 2571 | 17 | US-10-282-122A-24506 | | Sequence 24506, A |
| c | 40 | 120.4 | 7.8 | 5101 | 17 | US-10-398-221-3829 | | Sequence 3829, Ap |
| c | 41 | 120 | 7.8 | 2643 | 17 | US-10-282-122A-16514 | | Sequence 16514, A |
| | 42 | 117 | 7.6 | 117 | 17 | US-10-339-674-3370 | | Sequence 3370, Ap |
| c | 43 | 112 | 7.2 | 112 | 17 | US-10-339-674-3371 | | Sequence 3371, Ap |
| | 44 | 107.6 | 7.0 | 378 | 9 | US-09-974-300-1229 | | Sequence 1229, Ap |
| c | 45 | 103.8 | 6.7 | 639 | 17 | US-10-264-237-333 | | Sequence 333, App |

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OM nucleic - nucleic search, using sw model

Run on: May 22, 2005, 21:25:17 ; Search time 7780 Seconds
(without alignments)
7573.713 Million cell updates/sec

Title: US-10-733-776-1
Perfect score: 1548
Sequence: 1 tcgcgatctggtactgtaag.....tgatcgggtccgaagaagatc 1548

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result | | | % | | Query | | | | ID | Description |
|--------|-----|-------|-------|--------|-------|----------|---------|----|----------|-------------|
| | No. | Score | Match | Length | DB | DB | DB | DB | | |
| c | 1 | 821.4 | 53.1 | 847 | 9 | CL684250 | 2004 | | CL684250 | PRI0139a_ |
| | 2 | 776.8 | 50.2 | 812 | 9 | CL666243 | " | | CL666243 | PRI0151d_ |
| | 3 | 775 | 50.1 | 807 | 9 | CL666063 | " | | CL666063 | PRI0151b_ |
| c | 4 | 210.2 | 13.6 | 226 | 4 | BG382346 | low low | | BG382346 | 298212 MA |
| c | 5 | 191.2 | 12.4 | 752 | 9 | CL658545 | | | CL658545 | PRI0131d_ |
| c | 6 | 188.8 | 12.2 | 815 | 9 | CL693441 | | | CL693441 | PRI0161c_ |
| c | 7 | 177.8 | 11.5 | 837 | 9 | CL674143 | | | CL674143 | PRI0111b_ |
| | 8 | 168.8 | 10.9 | 2376 | 9 | CL982206 | | | CL982206 | OsIFSC046 |

| | | | | | | | | |
|---|----|-------|------|------|---|----------|----------|-------------|
| c | 9 | 167.6 | 10.8 | 2952 | 9 | CL982245 | CL982245 | OsIFSC047 |
| | 10 | 151 | 9.8 | 780 | 7 | CN586720 | CN586720 | USDA-FP_1 |
| | 11 | 133.6 | 8.6 | 1338 | 8 | BZ578038 | BZ578038 | msh2_569. |
| | 12 | 126 | 8.1 | 371 | 8 | BH404705 | BH404705 | AG-ND-120 |
| | 13 | 125.6 | 8.1 | 397 | 2 | AW983564 | AW983564 | RC3-HN000 |
| c | 14 | 104.6 | 6.8 | 828 | 9 | CL653278 | CL653278 | PRI0118a_ |
| | 15 | 101.4 | 6.6 | 103 | 8 | BH828707 | BH828707 | BACPP28-I |
| c | 16 | 100 | 6.5 | 545 | 4 | BJ619265 | BJ619265 | BJ619265 |
| c | 17 | 100 | 6.5 | 578 | 4 | BJ619554 | BJ619554 | BJ619554 |
| c | 18 | 99.6 | 6.4 | 764 | 9 | CL661098 | CL661098 | PRI0138d_ |
| | 19 | 98.6 | 6.4 | 725 | 4 | BJ446039 | BJ446039 | BJ446039 |
| | 20 | 98.6 | 6.4 | 726 | 4 | BJ437530 | BJ437530 | BJ437530 |
| | 21 | 98.2 | 6.3 | 543 | 4 | BJ440775 | BJ440775 | BJ440775 |
| | 22 | 97.6 | 6.3 | 706 | 4 | BJ436835 | BJ436835 | BJ436835 |
| c | 23 | 97.6 | 6.3 | 723 | 6 | C92149 | C92149 | C92149 Dict |
| | 24 | 97 | 6.3 | 614 | 4 | BJ434606 | BJ434606 | BJ434606 |
| c | 25 | 95.4 | 6.2 | 794 | 9 | CL666059 | CL666059 | PRI0151b_ |
| | 26 | 95.2 | 6.1 | 549 | 1 | AI857022 | AI857022 | MBNaAd-11 |
| | 27 | 95.2 | 6.1 | 805 | 9 | CL668572 | CL668572 | PRI0158a_ |
| c | 28 | 95 | 6.1 | 1222 | 8 | BZ572121 | BZ572121 | msh2_2521 |
| c | 29 | 94.8 | 6.1 | 1178 | 8 | BZ563590 | BZ563590 | pacs2-164 |
| | 30 | 94.4 | 6.1 | 411 | 1 | AI986973 | AI986973 | rs20b03.y |
| | 31 | 94.4 | 6.1 | 665 | 4 | BJ096681 | BJ096681 | BJ096681 |
| | 32 | 94.4 | 6.1 | 692 | 4 | BJ614351 | BJ614351 | BJ614351 |
| | 33 | 94.4 | 6.1 | 698 | 4 | BJ615952 | BJ615952 | BJ615952 |
| | 34 | 94.2 | 6.1 | 705 | 5 | BU725610 | BU725610 | SJMCFH11 |
| | 35 | 93 | 6.0 | 745 | 9 | CL683470 | CL683470 | PRI0137a_ |
| | 36 | 92.8 | 6.0 | 585 | 7 | CO250307 | CO250307 | WS00810.B |
| c | 37 | 92.6 | 6.0 | 846 | 9 | CL693676 | CL693676 | PRI0162b_ |
| | 38 | 92.6 | 6.0 | 868 | 7 | CK864671 | CK864671 | AGENCOURT |
| | 39 | 92.6 | 6.0 | 1258 | 9 | CG754091 | CG754091 | P049-2-F0 |
| | 40 | 92.6 | 6.0 | 1372 | 9 | CG749233 | CG749233 | P043-2-F0 |
| c | 41 | 92.2 | 6.0 | 649 | 7 | CF322664 | CF322664 | HDN--01-L |
| c | 42 | 91.8 | 5.9 | 672 | 4 | BJ787914 | BJ787914 | BJ787914 |
| | 43 | 91.6 | 5.9 | 498 | 1 | AT006939 | AT006939 | AT006939 |
| | 44 | 91.4 | 5.9 | 490 | 4 | BJ757406 | BJ757406 | BJ757406 |
| | 45 | 91.4 | 5.9 | 502 | 4 | BM279297 | BM279297 | Nb_ad1_05 |